

10\_578839 sequence listing (Q94769).TXT  
SEQUENCE LISTINGS

<110> INJE UNIVERSITY  
<120> CANCER CELL TARGETING GENE DELIVERY METHOD  
<130> Q94769  
<140> US 10/578,839  
<141> 2006-05-10  
<150> KR 10-2003-0079897  
<151> 2003-11-12  
<150> PCT/KR2004/000545  
<151> 2004-03-15  
<160> 11  
<170> KopatentIn 1.71  
<210> 1  
<211> 36  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> Env F primer  
  
<400> 1  
cgcggatccg aattccatac ctggtgttgc tgacta 36  
  
<210> 2  
<211> 47  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> 597LN primer  
  
<400> 2  
agctggacct ggctgccacc acctccgcta ttttgggtccc attttac 47  
  
<210> 3  
<211> 49  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> LC597 primer  
  
<400> 3  
caaccccgcc gcaggtggag gaggcagtga atggactcaa aaatttcaa 49  
  
<210> 4  
<211> 35  
<212> DNA

10\_578839 sequence listing (Q94769).TXT

<213> Artificial Sequence

<220>

<223> Spike R2 primer

<400> 4

tgctctagaa ttcttaaagg ttaccttcgt tctct

35

<210> 5

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> LnkNScFv primer

<400> 5

ggaggtggtg gcagccaggt ccagctagtg cagtct

36

<210> 6

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> ScFvLnkC primer

<400> 6

actgcctcct ccacctgcgg cgggggttgaa gtccca

36

<210> 7

<211> 2058

<212> DNA

<213> Gibbon Ape leukemia virus

<220>

<221> sig\_peptide

<222> (1)..(126)

<220>

<221> misc\_feature

<222> (127)..(1467)

<223> surface subunit region

<220>

<221> misc\_feature

<222> (1468)..(2025)

<223> transmembrain domain

<400> 7

atggtattgc tgcctgggtc catgcttctc acctcaaacc tgcaccacct tcggcaccag 60

atgagtcctg ggagctggaa aagactgata atcctcttaa gctgcgtatt cggcggcggc 120

gggacgagtc tgcaaaataa gaacccccac cagcccatga ccctcacttg gcagggtactg 180

10\_578839 sequence listing (Q94769).TXT

tcccaaactg	gagacgttgt	ctgggataca	aaggcagtcc	agcccccttg	gacttggtgg	240
cccacactta	aacctgatgt	atgtgccttg	gcggttagtc	ttgagtcctg	ggatatcccg	300
ggaaccgatg	tctcgtcctc	taaacgagtc	agacctccgg	actcagacta	tactgccgct	360
tataagcaaa	tcacctgggg	agccataggg	tgcagctacc	ctcgggctag	gactagaatg	420
gcaagctcta	ccttctacgt	atgtccccgg	gatggccgga	ccctttcaga	agctagaagg	480
tgcggggggc	tagaatccct	atactgtaaa	gaatgggatt	gtgagaccac	ggggaccggt	540
tattggctat	ctaaatcctc	aaaagacctc	ataactgtaa	aatgggacca	aaatagcgaa	600
tggactcaaa	aatttcaaca	gtgtcaccag	accggctggt	gtaacccccct	taaaatagat	660
ttcacagaca	aaggaaaatt	atccaaggac	tggataacgg	gaaaaacctg	gggattaaga	720
ttctatgtgt	ctggacatcc	aggcgtacag	ttcaccattc	gcttaaaaat	caccaacatg	780
ccagctgtgg	cagtaggtcc	tgacctcgtc	cttgtggaac	aaggacctcc	tagaacgtcc	840
ctcgctctcc	cacctcctct	tcccccaagg	gaagcgccac	cgccatctct	ccccgactct	900
aactccacag	ccctggcgac	tagtgcacaa	actcccacgg	tgagaaaaac	aattgttacc	960
ctaaacactc	cgctccccc	cacaggcgac	agactttttg	atcttggtgca	gggggccttc	1020
ctaaccttaa	atgctaccaa	cccagggggc	actgagtctt	gctggctttg	tttggccatg	1080
ggccccctt	attatgaagc	aatagcctca	tcaggagagg	tcgcctactc	caccgacctt	1140
gaccggtgcc	gctggggggc	ccaaggaaag	ctcacctca	ctgagggtctc	aggacacggg	1200
ttgtgcatag	gaaagggtgcc	ctttacccat	cagcatctct	gcaatcagac	cctatccatc	1260
aattcctccg	gagaccatca	gtatctgtc	ccctccaacc	atagctgggtg	ggcttgtagc	1320
actggcctca	ccccttgctt	ctccacctca	gtttttaatc	agactagaga	tttctgtatc	1380
cagggtccagc	tgattcctcg	catctattac	tatcctgaag	aagttttggtt	acaggcctat	1440
gacaattctc	accccaggac	taaaagagag	gctgtctcac	ttaccctagc	tgttttactg	1500
gggttgggaa	tcacggcggg	aatagggtact	ggttcaactg	ccttaattaa	aggacctata	1560
gacctccagc	aaggcctgac	aagcctccag	atcgccatag	atgctgacct	ccgggccctc	1620
caagactcag	tcagcaagtt	agaggactca	ctgacttccc	tgtccgaggt	agtgtctcaa	1680
aataggagag	gccttgactt	gctgtttcta	aaagaagggtg	gcctctgtgc	ggccctaaag	1740
gaagagtgtc	gtttttacat	agaccactca	ggtgcagtac	gggactccat	gaaaaaactc	1800
aaagaaaaac	tggataaaag	acagttagag	cgccagaaaa	gccaaaactg	gtatgaagga	1860
tggttcaata	actccccttg	gttcactacc	ctgctatcaa	ccatcgctgg	ggccctatta	1920
ctcctccttc	tgttgtcat	cctcgggcca	tgcatcatca	ataagttagt	tcaattcatc	1980
aatgatagga	taagtgcagt	taaaattctg	gtccttagac	aaaaatatca	ggccctagag	2040

aacgaaggta acctttaa

<210> 8  
 <211> 786  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> (346)..(390)  
 <223> (Gly4Ser)3 linker

<220>  
 <221> misc\_feature  
 <222> (739)..(777)  
 <223> PreS1 Tag

<400> 8  
 cagggtccagc tagtgcagtc tggggctgaa gtgaagaagc ctggggcttc agtgaagggtg 60  
 tcctgcaagg cttctggcta caccttcact gaccatgcaa ttactgggt gcgccaggcc 120  
 cctggacaac gccttgagtg gatgggatat ttttctcctg gcaacgatga ttttaaatac 180  
 tcccagaagt tccagggacg cgtgacaatc actgcagaca aatccgcgag cacagcctac 240  
 atggagctga gcagcctgag atctgaggac acggcgggtct attactgtgc aagatcggtg 300  
 aacatggcat actggggcca agggactctg gtcactgtct cttcagggtg aggcgggttca 360  
 ggcgagggtg gctctggcgg tggcggtatcg gacattgtga tgaccagtc tccagactcc 420  
 ctggctgtgt ctctgggcga gagggccacc atcaactgca agtccagcca gagtgtttta 480  
 tacagcagca acaataagaa ctacttagct tgggtaccagc agaaaccagg acagcctcct 540  
 aagctgctca ttactgggc atctacccgg gaatccgggg tccctgaccg attcagtggc 600  
 agcgggtctg ggacagattt cactctcacc atcagcagcc tgcaggctga agatgtggca 660  
 gtttattact gtcagcaata ttattcctat ccgttgacgt tcggccaagg gaccaagggtg 720  
 gaaatcaaag cggccgcagg agccaacgca aacaatccag attgggactt caaccccgcc 780  
 gcatag 786

<210> 9  
 <211> 13  
 <212> PRT  
 <213> PreS1 epitope at C-terminal of Tag-72pS1

<400> 9  
 Gly Ala Asn Ala Asn Asn Pro Asp Trp Asp Phe Asn Pro  
 1 5 10

<210> 10  
 <211> 2871  
 <212> DNA

## 10\_578839 sequence listing (Q94769).TXT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ScFv-GaLV Env GP chimeric peptide (FvGEL199) DNA

&lt;400&gt; 10

```

atggtattgc tgcctgggtc catgcttctc acctcaaacc tgcaccacct tcggcaccag 60
atgagtcctg ggagctggaa aagactgatc atcctcttaa gctgcgtatt cggcggcggc 120
gggacgagtc tgcaaaataa gaacccccac cagcccatga ccctcacttg gcaggtactg 180
tcccaaactg gagacgttgt ctgggataca aaggcagtc agcccccttg gacttggtgg 240
cccacactta aacctgatgt atgtgccttg gcggctagtc ttgagtcctg ggatatcccg 300
ggaaccgatg tctcgtcctc taaacgagtc agacctccgg actcagacta tactgccgct 360
tataagcaaa tcacctgggg agccataggg tgcagctacc ctcgggctag gactagaatg 420
gcaagctcta ctttctacgt atgtccccgg gatggccgga ccctttcaga agctagaagg 480
tgcggggggc tagaatccct atactgtaaa gaatgggatt gtgagaccac ggggaccggt 540
tattggctat ctaaatcctc aaaagacctc ataactgtaa aatgggacca aaatagcgga 600
ggtggtggca gccagggtcca gctagtgcag tctggggctg aagtgaagaa gcctggggct 660
tcagtgaagg tgtcctgcaa ggcttctggc tacaccttca ctgacctatgc aattcactgg 720
gtgcgccagg cccctggaca acgccttgag tggatgggat atttttctcc tggcaacgat 780
gattttaaat actcccagaa gttccagggc cgcgtgacaa tctactgcaga caaatccgcg 840
agcacagcct acatggagct gagcagcctg agatctgagg acacggcgggt ctattactgt 900
gcaagatcgt tgaacatggc atactggggc caagggactc tggtcactgt ctcttcaggt 960
ggaggcgggt caggcggagg tggctctggc ggtggcggat cggacattgt gatgaccag 1020
tctccagact ccctggctgt gtctctgggc gagagggcca ccatcaactg caagtccagc 1080
cagagtgttt tatacagcag caacaataag aactacttag ctggtacca gcagaaacca 1140
ggacagcctc ctaagctgct catttactgg gcatctaccc gggaatccgg ggtccctgac 1200
cgattcagtg gcagcgggtc tgggacagat ttcactctca ccatcagcag cctgcaggct 1260
gaagatgtgg cagtttatta ctgtcagcaa tattattcct atccgttgac gttcggccaa 1320
gggaccaagg tggaaatcaa agcggccgca ggagccaacg caaacaatcc agattgggac 1380
ttcaaccccg ccgaggtgg aggaggcagt gaatggactc aaaaatttca acagtgtcac 1440
cagaccggct ggtgtaaccc ccttaaaata gatttcacag acaaaggaaa attatccaag 1500
gactggataa cgggaaaaac ctggggatta agattctatg tgtctggaca tccaggcgta 1560
cagttcacca ttcgcttaaa aatcaccaac atgccagctg tggcagtagg tcctgacctc 1620
gtccttgtgg aacaaggacc tcctagaacg tccctcgctc tcccacctcc tcttccccca 1680

```

10\_578839 sequence listing (Q94769).TXT

```

agggaagcgc caccgccatc tctccccgac tctaactcca cagccctggc gactagtgca 1740
caaaactccca cgggtgagaaa aacaattgtt accctaataa ctccgcctcc caccacaggc 1800
gacagacttt ttgatcttgt gcagggggcc ttcctaacct taaatgctac caaccacagg 1860
gccactgagt cttgctggct ttgtttggcc atggggcccc cttattatga agcaatagcc 1920
tcatcaggag aggtcgccta ctccaccgac cttgaccggt gccgctgggg gacccaagga 1980
aagctcacc tcactgaggt ctcaggacac gggttgtgca taggaaagg ggcctttacc 2040
catcagcatc tctgcaatca gaccctatcc atcaattcct ccggagacca tcagtatctg 2100
ctcccccca accatagctg gtgggcttgc agcactggcc tcacccttg cctctccacc 2160
tcagttttta atcagactag agatttctgt atccagggtcc agctgattcc tcgcatctat 2220
tactatcctg aagaagtttt gttacaggcc tatgacaatt ctcaccccag gactaaaaga 2280
gaggctgtct cacttacct agctgtttta ctgggggttg gaatcacggc gggaaatagg 2340
actggttcaa ctgccttaat taaaggacct atagacctcc agcaaggcct gacaagcctc 2400
cagatcgcca tagatgctga cctccgggcc ctccaagact cagtcagcaa gttagaggac 2460
tcactgactt ccctgtccga ggtagtgctc caaaatagga gaggccttga cttgctgttt 2520
ctaaaagaag gtggcctctg tgcggcccta aaggaagagt gctgttttta catagaccac 2580
tcagggtgcag tacgggactc catgaaaaaa ctcaaaagaa aactggataa aagacagtta 2640
gagcgccaga aaagccaaaa ctggtatgaa ggatggttca ataactcccc ttggttcact 2700
accctgctat caaccatcgc tgggcccta ttactcctcc ttctgttgct catcctcggg 2760
ccatgcatca tcaataagtt agttcaattc atcaatgata ggataagtgc agttaaatt 2820
ctggtcctta gacaaaaata tcaggcccta gagaacgaag gtaaccttta a 2871

```

```

<210> 11
<211> 956
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> ScFv-GaLV Env GP chimeric ligand (FvGEL199)

```

```

<400> 11
Met Val Leu Leu Pro Gly Ser Met Leu Leu Thr Ser Asn Leu His His
 1           5           10           15
Leu Arg His Gln Met Ser Pro Gly Ser Trp Lys Arg Leu Ile Ile Leu
          20           25           30
Leu Ser Cys Val Phe Gly Gly Gly Gly Thr Ser Leu Gln Asn Lys Asn
          35           40           45
Pro His Gln Pro Met Thr Leu Thr Trp Gln Val Leu Ser Gln Thr Gly
          50           55           60

```

10\_578839 sequence listing (Q94769).TXT

Asp Val Val Trp Asp Thr Lys Ala Val Gln Pro Pro Trp Thr Trp Trp  
 65 70 75 80  
 Pro Thr Leu Lys Pro Asp Val Cys Ala Leu Ala Ala Ser Leu Glu Ser  
 85 90 95  
 Trp Asp Ile Pro Gly Thr Asp Val Ser Ser Ser Lys Arg Val Arg Pro  
 100 105 110  
 Pro Asp Ser Asp Tyr Thr Ala Ala Tyr Lys Gln Ile Thr Trp Gly Ala  
 115 120 125  
 Ile Gly Cys Ser Tyr Pro Arg Ala Arg Thr Arg Met Ala Ser Ser Thr  
 130 135 140  
 Phe Tyr Val Cys Pro Arg Asp Gly Arg Thr Leu Ser Glu Ala Arg Arg  
 145 150 155 160  
 Cys Gly Gly Leu Glu Ser Leu Tyr Cys Lys Glu Trp Asp Cys Glu Thr  
 165 170 175  
 Thr Gly Thr Gly Tyr Trp Leu Ser Lys Ser Ser Lys Asp Leu Ile Thr  
 180 185 190  
 Val Lys Trp Asp Gln Asn Ser Gly Gly Gly Gly Ser Gln Val Gln Leu  
 195 200 205  
 Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val  
 210 215 220  
 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His Ala Ile His Trp  
 225 230 235 240  
 Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met Gly Tyr Phe Ser  
 245 250 255  
 Pro Gly Asn Asp Asp Phe Lys Tyr Ser Gln Lys Phe Gln Gly Arg Val  
 260 265 270  
 Thr Ile Thr Ala Asp Lys Ser Ala Ser Thr Ala Tyr Met Glu Leu Ser  
 275 280 285  
 Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu  
 290 295 300  
 Asp Met Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly  
 305 310 315 320  
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile  
 325 330 335  
 Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg  
 340 345 350  
 Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn  
 355 360 365  
 Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro  
 370 375 380  
 Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp  
 385 390 395 400

10\_578839 sequence listing (Q94769).TXT

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser  
405 410 415

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr  
420 425 430

Ser Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ala  
435 440 445

Ala Ala Gly Ala Asn Ala Asn Asn Pro Asp Trp Asp Phe Asn Pro Ala  
450 455 460

Ala Gly Gly Gly Gly Ser Glu Trp Thr Gln Lys Phe Gln Gln Cys His  
465 470 475 480

Gln Thr Gly Trp Cys Asn Pro Leu Lys Ile Asp Phe Thr Asp Lys Gly  
485 490 495

Lys Leu Ser Lys Asp Trp Ile Thr Gly Lys Thr Trp Gly Leu Arg Phe  
500 505 510

Tyr Val Ser Gly His Pro Gly Val Gln Phe Thr Ile Arg Leu Lys Ile  
515 520 525

Thr Asn Met Pro Ala Val Ala Val Gly Pro Asp Leu Val Leu Val Glu  
530 535 540

Gln Gly Pro Pro Arg Thr Ser Leu Ala Leu Pro Pro Leu Pro Pro  
545 550 555 560

Arg Glu Ala Pro Pro Pro Ser Leu Pro Asp Ser Asn Ser Thr Ala Leu  
565 570 575

Ala Thr Ser Ala Gln Thr Pro Thr Val Arg Lys Thr Ile Val Thr Leu  
580 585 590

Asn Thr Pro Pro Pro Thr Thr Gly Asp Arg Leu Phe Asp Leu Val Gln  
595 600 605

Gly Ala Phe Leu Thr Leu Asn Ala Thr Asn Pro Gly Ala Thr Glu Ser  
610 615 620

Cys Trp Leu Cys Leu Ala Met Gly Pro Pro Tyr Tyr Glu Ala Ile Ala  
625 630 635 640

ser ser Gly Glu Val Ala Tyr Ser Thr Asp Leu Asp Arg Cys Arg Trp  
645 650 655

Gly Thr Gln Gly Lys Leu Thr Leu Thr Glu Val Ser Gly His Gly Leu  
660 665 670

Cys Ile Gly Lys Val Pro Phe Thr His Gln His Leu Cys Asn Gln Thr  
675 680 685

Leu Ser Ile Asn Ser Ser Gly Asp His Gln Tyr Leu Leu Pro Ser Asn  
690 695 700

His Ser Trp Trp Ala Cys Ser Thr Gly Leu Thr Pro Cys Leu Ser Thr  
705 710 715 720

Ser Val Phe Asn Gln Thr Arg Asp Phe Cys Ile Gln Val Gln Leu Ile  
725 730 735



10\_578839 sequence listing (Q94769).TXT

Pro	Arg	Ile	Tyr	Tyr	Tyr	Pro	Glu	Glu	Val	Leu	Leu	Gln	Ala	Tyr	Asp		
			740					745					750				
Asn	Ser	His	Pro	Arg	Thr	Lys	Arg	Glu	Ala	Val	Ser	Leu	Thr	Leu	Ala		
		755					760					765					
Val	Leu	Leu	Gly	Leu	Gly	Ile	Thr	Ala	Gly	Ile	Gly	Thr	Gly	Ser	Thr		
	770					775					780						
Ala	Leu	Ile	Lys	Gly	Pro	Ile	Asp	Leu	Gln	Gln	Gly	Leu	Thr	Ser	Leu		
	785				790					795					800		
Gln	Ile	Ala	Ile	Asp	Ala	Asp	Leu	Arg	Ala	Leu	Gln	Asp	Ser	Val	Ser		
				805					810					815			
Lys	Leu	Glu	Asp	Ser	Leu	Thr	Ser	Leu	Ser	Glu	Val	Val	Leu	Gln	Asn		
			820					825					830				
Arg	Arg	Gly	Leu	Asp	Leu	Leu	Phe	Leu	Lys	Glu	Gly	Gly	Leu	Cys	Ala		
		835					840					845					
Ala	Leu	Lys	Glu	Glu	Cys	Cys	Phe	Tyr	Ile	Asp	His	Ser	Gly	Ala	Val		
	850					855					860						
Arg	Asp	Ser	Met	Lys	Lys	Leu	Lys	Glu	Lys	Leu	Asp	Lys	Arg	Gln	Leu		
	865				870					875					880		
Glu	Arg	Gln	Lys	Ser	Gln	Asn	Trp	Tyr	Glu	Gly	Trp	Phe	Asn	Asn	Ser		
				885					890					895			
Pro	Trp	Phe	Thr	Thr	Leu	Leu	Ser	Thr	Ile	Ala	Gly	Pro	Leu	Leu	Leu		
			900					905					910				
Leu	Leu	Leu	Leu	Leu	Ile	Leu	Gly	Pro	Cys	Ile	Ile	Asn	Lys	Leu	Val		
		915					920					925					
Gln	Phe	Ile	Asn	Asp	Arg	Ile	Ser	Ala	Val	Lys	Ile	Leu	Val	Leu	Arg		
	930					935					940						
Gln	Lys	Tyr	Gln	Ala	Leu	Glu	Asn	Glu	Gly	Asn	Leu						
	945				950					955							